

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 03:23:15 ; Search time 96 Seconds
(without alignments)
5919.500 Million cell updates/sec

Title: US-09-315-355A-47

Perfect score: 1853
Sequence: 1 gatccctgagcgtgtgycag.....aaagaattcctaact 1853

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5a.COMB.seq:*
2: /cgn2_6/prodata/2/ina/5a.COMB.seq:*
3: /cgn2_6/prodata/2/ina/5a.COMB.seq:*
4: /cgn2_6/prodata/2/ina/5a.COMB.seq:*
5: /cgn2_6/prodata/2/ina/5a.COMB.seq:*
6: /cgn2_6/prodata/2/ina/5a.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	62.2	3.4	7218	1 US-08-232-463-14	Sequence 14, Appl
2	48.4	2.6	2518	4 US-09-433-699-3	Sequence 3, Appl
3	44.8	2.4	3925	2 US-09-047-026A-3	Sequence 3, Appl
4	42.2	2.3	1958	4 US-09-702-327-3	Sequence 3, Appl
5	42.2	2.3	2295	1 US-08-375-300-3	Sequence 3, Appl
6	42.2	2.3	2295	3 US-09-177-431-3	Sequence 3, Appl
7	42.2	2.3	2295	5 PCT-US95-16930-3	Sequence 3, Appl
8	42.2	2.3	4080	1 US-08-375-300-1	Sequence 1, Appl
9	42.2	2.3	4080	5 US-09-177-431-1	Sequence 1, Appl
10	42.2	2.3	4080	5 PCT-US95-16930-1	Sequence 1, Appl
11	41.8	2.3	666	4 US-08-998-416-1050	Sequence 1050, Ap
12	41.8	2.3	3489	2 US-08-728-323A-1	Sequence 1, Appl
13	41.8	2.3	3489	4 US-05-298-568-1	Sequence 1, Appl
14	41.8	2.3	32207	4 US-08-770-379-20	Sequence 20, Appl
C 15	41.8	2.3	32207	4 US-08-757-669A-20	Sequence 20, Appl
C 16	41.8	2.3	32207	4 US-09-230-371A-20	Sequence 20, Appl
C 17	41.8	2.3	32207	4 US-08-676-967-2	Sequence 2, Appl
18	40	2.2	2277	1 US-08-676-967-2	Sequence 2, Appl
19	40	2.2	2277	1 US-09-098-487-2	Sequence 2, Appl
20	39.8	2.1	1242	1 US-08-252-966B-13	Sequence 13, Appl
21	39.2	2.1	14855	2 US-08-687-080-59	Sequence 59, Appl
22	38	2.1	289	4 US-09-007-005-17	Sequence 17, Appl
23	38	2.1	289	4 US-09-244-796-17	Sequence 17, Appl
24	37.4	2.0	1221	2 US-08-658-665-55	Sequence 55, Appl
25	37.4	2.0	1221	4 US-08-796-101-19	Sequence 19, Appl
26	37.4	2.0	1221	4 US-09-085-273-55	Sequence 55, Appl
27	37.4	2.0	1221	4 US-09-171-699-3	Sequence 3, Appl

28	37.4	2.0	1221	5 PCT-US94-02107-1	Sequence 1, Appl
29	37.4	2.0	1383	4 US-08-658-665-58	Sequence 58, Appl
30	37.4	2.0	1383	4 US-08-796-101-22	Sequence 22, Appl
31	37.4	2.0	1383	4 US-09-085-273-58	Sequence 58, Appl
32	37.4	2.0	1386	2 US-08-658-665-53	Sequence 53, Appl
33	37.4	2.0	1386	4 US-08-796-101-17	Sequence 17, Appl
34	37.4	2.0	1386	4 US-09-085-273-53	Sequence 53, Appl
35	37.4	2.0	1476	2 US-08-658-665-50	Sequence 50, Appl
36	37.4	2.0	1476	4 US-08-796-101-14	Sequence 14, Appl
37	37.4	2.0	1476	4 US-09-085-273-50	Sequence 50, Appl
38	37.4	2.0	1975	2 US-08-658-665-51	Sequence 51, Appl
C 39	37.4	2.0	1975	4 US-08-796-101-15	Sequence 15, Appl
C 40	37.4	2.0	1975	4 US-09-085-273-51	Sequence 51, Appl
41	37.4	2.0	2225	1 US-08-450-945-56	Sequence 56, Appl
42	37.4	2.0	2225	4 US-08-976-161-56	Sequence 56, Appl
43	37.4	2.0	2314	3 US-08-105-454-1	Sequence 1, Appl
44	37.4	2.0	2577	2 US-08-658-665-56	Sequence 56, Appl
45	37.4	2.0	2577	4 US-08-796-101-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTgpt-Fls
US-08-232-463-14
Query Match 3.4% Score 62.2 DB 1; Length 7218;

784 GTTCCGTGGAAGCCAGACGTGGCTGAGGATGAGATGAAGAAGAGGATGATGAGGAC 843

3655 TGAGCAATATCAGAGAAATGATGAGGAGGAGACACATATGAAGAAGACAGT

RESULT 4

MOLECULE TYPE: DNA

Matches	107;	conservative	0;	mismatches	106;	indels	0;	gaps	0;
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212 AATTGCAAGAGAAGGTGGTGGCAGTGATGAAGAGGAGACAGGCAGTCTTCAGAGATG 271

Db 1595 ATTACTAGAGGAGGAGATGAGACCCGGAGATTAACACCCAGACAGAGTACAGCCAG 1654
 Oy 272 GCATGACAGAGTGCACGACCCAGCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
 Db 1555 GAAACATCTACGAGCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1714
 Oy 332 AGATGACAG 391
 Db 1715 ATGATGACAGATGAG 1774
 Oy 392 AGGAGGTGACCCAGATGCTGAGACTCTTGCTGAA 426
 Db 1775 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1809

RESULT 7 PCT-US95-16930-3

; Sequence 3, Application PC/TUS9516930
 ; GENERAL INFORMATION:
 ; APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
 ; TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE
 ; TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
 ; TITLE OF INVENTION: NONSENSE-MEDIATED MRNA DECAY
 ; TITLE OF INVENTION: FUNCTION
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street Suite 3100
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/16930
 ; FILING DATE: 27-DEC-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/375,300
 ; FILING DATE: 20-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 04020/046M01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)542-5070
 ; TELEFAX: (617)542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2295 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; PCT-US95-16930-3

Query Match 2.3%; Score 42.2; DB 5; Length 2295;
 Best Local Similarity 49.8%; Pred. No. 0.03;
 Matches 107; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Oy 212 AATTGCAAGAAGAGGTGGCGAGTATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
 Db 1595 ATTACTAG 1654
 Oy 272 GCATGACAGAGTGCACGACCCAGCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
 Db 1655 GAAACATCTACGAGCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1714

Oy 332 AGATGACAG 391
 Db 1715 ATGATGACAGATGAG 1774
 Oy 392 AGGAGGTGACCCAGATGCTGAGACTCTTGCTGAA 426
 Db 1775 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1809

RESULT 8 US-08-375-300-1

; Sequence 1, Application US/08375300
 ; Patent No. 5679566
 ; GENERAL INFORMATION:
 ; APPLICANT: Feng, He
 ; APPLICANT: Jacobson, Allan S.
 ; TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
 ; TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street Suite 3100
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/375,300
 ; FILING DATE: 20-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. P.
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 04020/046001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)542-5070
 ; TELEFAX: (617)542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4080 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-375-300-1

Query Match 2.3%; Score 42.2; DB 1; Length 4080;
 Best Local Similarity 49.8%; Pred. No. 0.041;
 Matches 107; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Oy 212 AATTGCAAGAAGAGGTGGCGAGTATGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
 Db 3044 ATTACTAG 3103
 Oy 272 GCATGACAGAGTGCACGACCCAGCCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
 Db 3104 GAAACATCTACGAGCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3163
 Oy 332 AGATGACAG 391
 Db 3164 ATGATGACAGATGAG 3223
 Oy 392 AGGAGGTGACCCAGATGCTGAGACTCTTGCTGAA 426
 Db 3224 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3258

RESULT 9

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1  TITLE OF INVENTION: FUNCTION.
2  NUMBER OF SEQUENCES: 6
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Fish & Richardson
5  STREET: 225 Franklin Street Suite 3100
6  CITY: Boston
7  STATE: MA
8  COUNTRY: USA
9  ZIP: 02110-2804
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: PCT/US95/16930
17 FILING DATE: 27-DEC-1995
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/375,300
20 FILING DATE: 20-JAN-1995
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Fasse, J. Peter
23 REGISTRATION NUMBER: 32,983
24 REFERENCE/DOCKET NUMBER: 04020/046W01
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (617)542-5070
27 TELEFAX: (617)542-8906
28 TELEX: 200154
29 INFORMATION FOR SEQ ID NO: 1:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 4080 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: DNA
36 PCT-US95-16930-1
37
38 Query Match 2.3%; Score 42.2; DB 5; length 4080;
39 Best Local Similarity 49.8%; Pred. No. 0.041;
40 Matches 107; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
41
42 Oy 212 AATTCCAGAGAGAGCTGTGGCACTGATGGAAGAGAGACAGCGACTCTTCAGAAAGTG 271
43 Db 3044 ATTACTCTGAGGAAAGATGAAGACGGCGAGATAGTACACCGAAGCAGAGTACGGCCAG 3103
44 Oy 272 GCATCGACAAGTCAGCAGCACCAGCAGCAGCCCAAGAGAGACCCCTGGAGAGATGGTGAACCG 331
45 Db 3104 GAAACATCATGAGCAAGCAAGCAAGCAAGCAAGTGAAGATGAAGAGATAGGAGCATGACGAGG 3163
46 Oy 332 AGGATGACAGCAGCGCTTGATGATGATGAGACCTGCTGAGTAGCAGCTTAATAATATGATG 391
47 Db 3164 ATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3223
48 Oy 392 AGGAGGTGACCCAGATGCTGAGATCTTGATGATGATGATGATGATGATGATGATGATGATG 426
49 Db 3224 ATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3258
50
51 RESULT 11
52 US-08-998-416-1050
53 Sequence 1050, Application US/08998416
54 Patent No. 6239264
55
56 GENERAL INFORMATION:
57 APPLICANT: Philippsen, Peter
58 APPLICANT: Pohlmann, Rainer
59 APPLICANT: Steiner, Sabine
60 APPLICANT: Mohr, Christine
61 APPLICANT: Wendland, Jurgen
62 APPLICANT: Knechtle, Philipp
63 APPLICANT: Redlschning, Corinne
64 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII
65 TITLE OF INVENTION: AND USES THEREOF
66 NUMBER OF SEQUENCES: 1152

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COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3489
US-08-728-323A-1

Query Match      2.3%   Score 41.8; DB 2; Length 3489;
Best Local Similarity 47.8%; Freq. No. 0.049;
Matches 121; Conservative 0; Mismatches 132; Indels 0; Gaps 0.

QY 173 AAGAAGAGTAATAAACGCCCTATTCGTGAGGGCAAGAGAAATTGCACGAAGAAGTGTG 232
    |||||
DB 989 ATGATGACGAGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1048
    |||||

QY 233 GCAGTGATGAAGAGAGACAGCAGCAGTCCCTTCAGAAAGATGGCATGCAGAGTGCACGCACC 292
    |||||
DB 1049 AGGAGAGTAGCAGCAGGAGCGATGACGAGGAGGAGATGACGAGCAGCATGACGAGGAGATGACG 1108
    |||||

QY 293 AGGCACGGCCCAAAGAGAGCCCCGTGGAGATGCTGACCCAGAGAGATGACAGGAGCGTTGATG 352
    |||||
DB 1109 AGGAGAGTAGCAGCAGGACGATGACGAGGAGATGACGAGGAGATGACGAGGAGAGAGACG 1168
    |||||

QY 353 ATGATGACCTGGCTGACTGACGACTTATGATTAATATGATGAGGAAGGTGACCCAGATGCTG 412
    |||||
DB 1169 AGGAGAGTAGCAGCAGGAGAGGACGAGGAGGAGAGGAGAGGAGAGGAGATGACGATGATGTAAG 1228
    |||||

QY 413 AGACTCTTGTGCA 425
    |||||
DB 1229 ACAATGAGGACGA 1241

RESULT 13
US-09-298-568-1
Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
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LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

Query Match 2.3%, Score 41.8; DB 4; Length 3489;
Best Local Similarity 47.8%; Pred. No. 0.049;
Matches 121; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

173 AAGAAGAGTAAACGCTCATTTGCTGAGCCAAAGAGAAATTGCAAGAGAGTGGTG 232
DB 989 ATGATGAG 1048
233 GCAGTGAATGAAG 292
DB 1049 AGGAGAGTACAG 1108
293 AGGACAGCCCAAG 352
DB 1109 AGGAGAGTACAG 1168
353 ATGATGAGAGTGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
DB 1169 AGGAG 1228
413 AGACTCTTGCTGA 425
DB 1229 ACAATGAGAGACGA 1241

RESULT 14
US-08-770-379-20/c
Sequence 20, Application US/08770379
Patent No. 5849564

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-770-379-20

Query Match 2.3%, Score 41.8; DB 2; Length 32207;
Best Local Similarity 47.8%; Pred. No. 0.15;
Matches 121; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

173 AAGAAGAGTAAACGCTCATTTGCTGAGCCAAAGAGAAATTGCAAGAGAGTGGTG 232
DB 21008 ATGATGAG 20949
233 GCAGTGAATGAAG 292
DB 20948 AGGAGAGTACAG 20889
293 AGGACAGCCCAAG 352
DB 20888 AGGAGAGTACAG 20829
353 ATGATGAGAGTGGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 412
DB 20828 AGGAG 20769
413 AGACTCTTGCTGA 425
DB 20768 ACAATGAGAGACGA 20756

RESULT 15
US-08-757-669A-20/c
Sequence 20, Application US/08757669A
Patent No. 6183751

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20
Query Match 2.3%, Score 41.8; DB 4; Length 32207;

Best Local Similarity 47.88; Pred. No. 0.15;
Matches 121; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Accession	Sequence	Position
Oy 173	AGGAAGAAGTAAAGCCCTCATTGCTGAGGCAAAAGAGAAATTCGAAGAAGAAGGTGGT	232
Db 21008	ATGATGAGAGAGAGACGACGACAGTATGAGAGACGAGAGAGATACGAGGAGATGACG	20949
Oy 233	GCATGTATGAAGAGAGACACAGGCACTCCTTCGAAGATGGCATGCAGATGCACACACC	292
Db 20948	AGGAGAGATACGACGAGAGATGACGAGAGATGACGAGAGAGATGACGAGAGATGACG	20889
Oy 293	AGGCACGGCCAAAGAGGCCCTCGAGAGATGGTGACCCAGAGAGATGACAGACGCTTGATG	352
Db 20888	AGGAGGATGACGACGAGAGCATGACGAGGAGAGATGACGAGAGAGATGACGAGAGAGACG	20829
Oy 353	ATGATGAGCTGGCTGAGTACGACTTAAATATATGATGAGAGAAAGTACCAGATGCTG	412
Db 20838	AGGAGAGAGACGAGAGAGAGAGACGAGAGAGAGAGAGAGAGAGATGCGATGTAGAG	20769
Oy 413	AGACTCTGGTGA 425	
Db 20768	ACAATGAGACGA 20756	

Search completed: May 22, 2003, 22:44:59
Job time : 230 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: May 22, 2003, 22:43:09 ; Search time 244 Seconds
(without alignments)
10027.937 Million cell updates/sec

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Title: US-09-315-355A-47
Perfect score: 1853
Sequence: 1 gatccctgagcgtgtgacag.....aaagtaattccttaacat 1853
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%

Database

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1: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq.*
Published.Applications.NA.*
2: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubnpa/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubnpa/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubnpa/PCMS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubnpa/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubnpa/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubnpa/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubnpa/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubnpa/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubnpa/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubnpa/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	459.4	24.8	508	9	US-09-918-995-21467	Sequence 21467, A
2	150	8.1	150	10	US-09-860-107-2725	Sequence 2725, A
3	53.2	2.9	2895	9	US-09-938-842A-2540	Sequence 2540, Ap
4	52.8	2.8	766	10	US-09-864-761-19608	Sequence 19608, A
5	52.8	2.8	1944	10	US-09-864-761-2825	Sequence 2825, Ap
6	49	2.6	1959	10	US-09-864-761-4012	Sequence 4012, A
7	47.8	2.6	583	10	US-09-864-761-20772	Sequence 20772, A
8	47	2.5	1626	9	US-10-116-016-19	Sequence 19, Appl
9	47	2.5	1626	9	US-10-103-313-271	Sequence 271, Appl
10	47	2.5	1626	10	US-09-764-848-19	Sequence 19, App
11	47	2.5	2648	9	US-10-103-313-158	Sequence 158, App
12	46.6	2.5	1184	9	US-10-123-155-412	Sequence 412, App
13	46.2	2.5	58985	9	US-09-901-152-3	Sequence 3, Appl1
14	44.6	2.4	439	10	US-09-864-761-20174	Sequence 20174, A
15	44.2	2.4	2142	10	US-09-917-800A-1567	Sequence 1567, Ap
16	43.8	2.4	888	10	US-09-770-445-502	Sequence 502, Appl
17	43.6	2.4	327	10	US-09-864-761-28059	Sequence 28059, A
18	43.6	2.4	575	10	US-09-864-761-20733	Sequence 20733, A
19	43.6	2.4	1969	10	US-09-864-761-3972	Sequence 3972, Ap

ALIGNMENTS

C 20	43.3	2.3	720	9	US-10-101-487-74	Sequence 74, Appl
C 21	43.4	2.3	720	9	US-10-101-487-76	Sequence 76, Appl
C 22	43	2.3	8895	9	US-10-091-438-250	Sequence 250, App
C 23	43	2.3	8895	9	US-10-091-438-256	Sequence 256, App
C 24	43	2.3	8895	10	US-09-764-853-887	Sequence 887, App
C 25	43	2.3	8895	10	US-09-764-853-937	Sequence 937, App
C 26	43	2.3	9656	9	US-10-091-438-246	Sequence 246, App
C 27	43	2.3	9656	9	US-10-091-438-255	Sequence 255, App
C 28	43	2.3	9656	10	US-09-764-853-886	Sequence 886, App
C 29	43	2.3	9656	10	US-09-764-853-933	Sequence 933, App
C 30	42.8	2.3	522	9	US-10-101-487-71	Sequence 71, Appl
C 31	42.8	2.3	530	9	US-10-101-487-73	Sequence 73, Appl
C 32	42.8	2.3	554	9	US-10-101-487-69	Sequence 69, Appl
C 33	42.8	2.3	554	9	US-10-101-487-106	Sequence 106, App
C 34	42.4	2.3	565	10	US-09-864-761-663	Sequence 663, App
C 35	42.2	2.3	431	9	US-09-918-995-15180	Sequence 15180, A
C 36	42.2	2.3	1251	9	US-09-828-000-1	Sequence 1, Appl
C 37	42.2	2.3	1920	9	US-09-906-393A-35	Sequence 35, Appl
C 38	42.2	2.3	1958	10	US-09-791-406-3	Sequence 3, Appl
C 39	42.2	2.3	110096	10	US-09-880-107-1552	Sequence 1542, App
C 40	41.4	2.2	460	10	US-09-864-761-2587	Sequence 2587, App
C 41	41.4	2.2	566	10	US-09-864-761-98	Sequence 98, Appl
C 42	41.4	2.2	582	10	US-09-864-761-8188	Sequence 8188, App
C 43	41.2	2.2	475	10	US-09-864-761-1361	Sequence 1361, App
C 44	41.2	2.2	512	10	US-09-864-761-18121	Sequence 18121, A
C 45	40.4	2.2	345	10	US-09-822-263-7	Sequence 7, Appl

Query Match	Best Local Similarity	Matches	Conservative	n = A,T,C or G	24.8%	Score 459.4	DB 9	Length 508
QY 1354	GTTCATTCTAGGAGCATGAAATGGGAGCTTCCTCTGTTCTTCATGTCGCCGTATTTG	1413	98.7%	Pred. 0	Mismatches 6	Indels 0	Gaps 0	
DB 40	GTTCATTCTAGGAGCATGCAATGGGAGCTTCCTCTGTTCTTCATGTCGCCGTATTTG	99	0	0	0	0	0	
QY 1414	CCATTATTTATGCTTTGGAGGTCAAAAAAGAGGCTTCGGGCTCGGATATTAAGCACA	1473	98.7%	Pred. 0	Mismatches 6	Indels 0	Gaps 0	
DB 100	CCATTATTTATGCTTTGGAGGTCAAAAAAGAGGCTTCGGGCTCGGATATTAAGCACA	159	0	0	0	0	0	
QY 1474	GTCCTTCAGTAAAGAGCATTTGGAGACGACGAGAGGCTTCCTGTTGGAGTGAACA	1533	98.7%	Pred. 0	Mismatches 6	Indels 0	Gaps 0	
DB 160	GTCCTTCAGTAAAGAGCATTTGGAGACGACGAGAGGCTTCCTGTTGGAGTGAACA	219	0	0	0	0	0	
QY 1534	AATTCATCTATTATGAGCCCTTTTGGACGACGAGCTCGATACACCCATGAGAGTCTTAA	1593	98.7%	Pred. 0	Mismatches 6	Indels 0	Gaps 0	

RESULT 3
US-09-9398-842A-2540
Sequence 2540, Application US/0993842A
Patent No. US20020169378A1
GENERAL INFORMATION:
APPLICANT: Halper, Jeff
APPLICANT: Kleps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong

RESULT 4
 US-09-864-761-19608/c
 Sequence 19608, Application US/09864761
 Patent No. US20020048763a1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04

[illegible]

Query Match	2.8%	Score 52.8;	DB 10;	Length 1944;
Best Local Similarity	48.1%;	Pred. No. 8.8e-05;		
Matches .150;	Conservative 0;	Mismatches 162;	Indels 0;	Gaps 0;
<p>320 ATGTGACCCAGAGAGTACAGAGCGCTTGATGATGATGATGAGCTGGCTGACATGCACTTAG 379</p>				

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Db 562 ATGTGCAATGTAATGATGATGATGAGGAGGAGGAGGAGGATGATGATGATGATGATG 503
Qy 380 ATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 439
Db 502 ATGATGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 443
Qy 440 TTACGCTTCACGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
Db 442 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 383
Qy 500 ATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 559
Db 382 ATGAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 323
Qy 560 AACAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 619
Db 322 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 263
Qy 620 TACACCATGATA 631
Db 262 ATGCTGATGATA 251

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RESULT 6
US-09-864-761-4012

; Sequence 4012, Application US/09864761
; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aecmca-x-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263,6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

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; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4012
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022334.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; US-09-864-761-4012

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Query Match 2.64; Score 49; DB 10; Length 1959;
Best Local Similarity 45.64; Pred. No. 0.0012;
Matches 172; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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Qy 317 AGATGCTGACCCAGAGATGACAGACGCTGTGATGATGATGATGATGATGATGATGATG 376
Db 388 ATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 447
Qy 377 TAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 436
Db 448 ATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
Qy 437 GCTTACGCTGCTACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 496
Db 508 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567
Qy 497 AATATGACGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
Db 568 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627
Qy 557 CTGACAGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 616
Db 628 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687
Qy 617 ATGTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 676
Db 688 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 747
Qy 677 ATCCTAGCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 693
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RESULT 7

US-09-864-761-20772

; Sequence 20772, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Aecmca-x-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

Db 372 GAATATATAGAAAGAAATCTGATGTCGAATATGATGATTTGGACGTAAGAAAGAA 431
QY 268 GATGCGATGCGAGTGCACGCGACGCCCAAGAGAGCCCTGGAGATGTCAC 327
Db 432 AAATTCAGAGGGAAGAGAGGTTGCTGTCATCTATATTAAGAGAGTTGAAGATAAGAA 491
QY 328 CCAGAGGATGACAGAGCGCTTGATGATGATGATGATGATGATGATGATGATGATGAT 387
Db 492 TCAGAGGAGAGAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
QY 388 GATGAGGAGGATGACCCAGAT 408
Db 552 GAGGATGAGATGACGCTGAT 572

RESULT 10

US-09-764-848-19
; Sequence 19, Application US/09764848
; Patent No. US20020077270A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT208
; CURRENT APPLICATION NUMBER: US/09/764,848
; PRIOR APPLICATION DATA REMOVED - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-848-19

Query Match 2.5%; Score 47; DB 10; Length 1626;
Best Local Similarity 51.7%; Pred. No. 0.0043;
Matches 104; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

QY 208 GAGAAATTCAGAGAGAGGTGGTGGCAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
Db 372 GAATATATAGAAAGAGAGATCTGATGTCGAATATGATGATGATGATGATGATGATGATGAT 431
QY 268 GATGCGATGCGAGTGCACGCGACGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
Db 432 AAATTCAGAGGGAAGAGAGGTTGCTGTCATCTATATTAAGAGAGTTGAAGATAAGAA 491
QY 328 CCAGAGGATGACAGAGCGCTTGATGATGATGATGATGATGATGATGATGATGATGAT 387
Db 492 TCAGAGGAGAGAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
QY 388 GATGAGGAGGATGACCCAGAT 408
Db 552 GAGGATGAGATGACGCTGAT 572

RESULT 11

US-10-103-313-158
; Sequence 158, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P20701
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 158
; LENGTH: 2648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-158

Query Match 2.5%; Score 47; DB 9; Length 2648;
Best Local Similarity 51.7%; Pred. No. 0.0061;
Matches 104; Conservative 1; Mismatches 96; Indels 0; Gaps 0;

QY 208 GAGAAATTCAGAGAGAGGTGGTGGCAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
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QY 268 GATGCGATGCGAGTGCACGCGACGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
Db 445 AAATTCAGAGGGAAGAGAGGTTGCTGTCATCTATATTAAGAGAGTTGAAGATAAGAA 504
QY 328 CCAGAGGATGACAGAGCGCTTGATGATGATGATGATGATGATGATGATGATGATGAT 387
Db 505 TCAGAGGAGAGAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 564
QY 388 GATGAGGAGGATGACCCAGAT 408
Db 565 GAGGATGAGATGACGCTGAT 585

RESULT 12

US-10-123-155-412
; Sequence 412, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: * Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 412
; LENGTH: 1184
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-412

Query Match 2.5%; Score 46.6; DB 9; Length 1184;
Best Local Similarity 8.9%; Pred. No. 0.0045;
Matches 59; Conservative 191; Mismatches 411; Indels 0; Gaps 0;

QY 330 AGAGATGACAGAGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 389
Db 319 ARRAGOSVSLCCCKATGPRPDKYFWYHNDLIDPSLYKHESKYLVRKLOOHQAGEYFCA 378
QY 390 TGAGGAAGTGCACCGAGTCTGAGACTCTGCTGATGATGATGATGATGATGATGATGATGAT 449
Db 379 OSDAGAVKSVKQILVYASDETPCNPPEYSYLIRLPHDCQONATNSFYDVGKPVKTCA 438
QY 450 CGGAGTAATGATCAAGATCCTTACTGATGATGATGATGATGATGATGATGATGATGATGAT 509
Db 439 GQDNDGIRCDNAVQNCGISKTERELQCSGYLLPFRKVAKEGCGQCTERISIVRQVNA 498

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QY 510 AGATCTTCGATTAAAGCCAGTATATCTTATAGTTTGCGCCAGCTGAACAGACCA 569
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 499 ADNGEMRGRGHYMGSRISMTGYKCTFLHVPQDTERLVLTFRVYLQKRVNTTKLPPN 558
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 570 GTGCAATTTAGAGGTGCATGTTTATATCAAGAAAGACTCTTTTATGATCACCATGA 629
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 559 KGSAAVEHEIKMLRKEPTILEAMETNIIPLGEVGEDPMALIEIPSRFYRQNGEPYIG 618
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 630 TATACCTTGTCGCTATACCTCTGAGTGTGATGGCTGAATTTGATCTTACCCAGA 669
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 619 KVKASVTFLLPNNIATAAQTDLNFINDEGDTFLRTYGMFVDRDEVTSEPLNAGKY 678
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 690 TGATTTACTGGAATTTACATGCTGTAGGAAGAACATGACCCCGTATATGAAGTGGGA 749
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 679 KHLBDSTQVKMEPHISTVILWMSLNPTGLMEEGDKRFENQRNKKEDRFLVGNLEIRE 738
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 750 CCTTGATATAGTGAGCTCTTGAAGCCAGTCTTACACTCGAAGTAATCTTCAAAAA 809
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 739 RLLENLDVDESRCFVKVAVRSEFLPSEIQGVIVSYINLEPRIGLSNPRAMGRPDS 798
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 810 GAAGAAAAAGAAAGAAAGAGTCTCAGACAGAGGACATACCGATGCTCTTGA 869
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 799 VTGPGACVPAFCDDQSPDAYSAYVLASLAGEELQAVSSPFPNPAIGVPPQYLKLN 858
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 870 CCTTGATGAATTAAGCTATATCAGAAATGTTTACGCAAGTGCATGACCTGACAACTGT 929
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 859 YRTDIEDHVRKTAFOISMARPRPSAESNPITAFENLRACEAPPSAAHFRYQTE 918
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 930 AATCTGTGGATATGCTCTTGGGAAACAGCAGCTAGCTGCTGACACAGACAA 969
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 919 GDRYDNTVPFNEDDPMSTEDYLAMPKPMERPRACYIKVKIYGLEVVNRSNMGGTHR 978
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QY 990 G 990
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DB 979 R 979
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RESULT 13

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US-09-901-152-3/c
; Sequence 3, Application US/09901152
; Publication No. US20030022824A1
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001248
; CURRENT APPLICATION NUMBER: US/09/901,152
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 58985
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(58985)
; OTHER INFORMATION: n - A,T,C or G
US-09-901-152-3
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Query Match 2.5%; Score 46.2; DB 9; Length 58985;
Best Local Similarity 50.7%; Pred. No. 0.097;
Matches 111; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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QY 319 GATGTGACCCAGAGATGACAGAGCTTGATGATGATGAGCTGCTGAGTACGACTTA 378
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11221 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11162
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 379 GATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 438
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11161 GGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11102
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 439 CTTACGTCACGGAGATATGATCAAGATCCTTACGTTACTCTGAAGATACAGAAC 498
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11101 GATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11042
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 499 TATGAACGTGACAGATCTTCTGATTAAGCCAGTATAT 537
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11041 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11003
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 14

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US-09-864-761-20174/c
; Sequence 20174, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20174
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL035419.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
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